



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/922,240  
Source: IFW16  
Date Processed by STIC: 7/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>08/922,240</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. <b>Do not use tab codes between numbers; use space characters</b> , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was <b>not saved</b> in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If <b>intentional</b> , please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the <b>only valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can <b>only</b> represent a single <u>nucleotide</u> ; "Xaa" can <b>only</b> represent a single <u>amino acid</u>	



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004

TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT

Output Set: N:\CRF4\07232004\H922240.raw

4 <110> APPLICANT: Schreiber, Stuart L.  
 5       Belshaw, Peter  
 6       Crabtree, Gerald R.  
 8 <120> TITLE OF INVENTION: GENE THERAPY BY CELL SPECIFIC TARGETING  
 11 <130> FILE REFERENCE: APBI-P01-007  
 13 <140> CURRENT APPLICATION NUMBER: US 08/922,240  
 14 <141> CURRENT FILING DATE: 1997-08-27  
 16 <150> PRIOR APPLICATION NUMBER: US 60/024,666  
 17 <151> PRIOR FILING DATE: 1996-08-27  
 19 <160> NUMBER OF SEQ ID NOS: 3  
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 10  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Unknown  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Peptide  
 W--> 31 <221> NAME/KEY: VARIANT  
 32 <222> LOCATION: 1  
 33 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid  
 W--> 35 <221> VARIANT  
 36 <222> LOCATION: 2  
 37 <223> OTHER INFORMATION: Xaa = Sar: sarcosine  
 W--> 39 <221> VARIANT  
 40 <222> LOCATION: 3, 5, 8, 9  
 41 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine  
 W--> 43 <221> VARIANT  
 44 <222> LOCATION: 7  
 45 <223> OTHER INFORMATION: Xaa = D-Ala: D-alanine  
 W--> 47 <221> VARIANT  
 48 <222> LOCATION: 10  
 49 <223> OTHER INFORMATION: Xaa = Ac-N-MeValinol ester  
 W--> 51 <400> 1  
 W--> 52 Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa Xaa  
 53   1                   5                           10  
 56 <210> SEQ ID NO: 2  
 57 <211> LENGTH: 12  
 58 <212> TYPE: PRT  
 59 <213> ORGANISM: Unknown  
 61 <220> FEATURE:  
 62 <223> OTHER INFORMATION: Peptide  
 W--> 64 <221> NAME/KEY: VARIANT  
 65 <222> LOCATION: 1

pp 1-3  
 Basic Info: Simply  
 identifying the compound.

Understood - please attempt to give  
 source of genetic  
 material as explanation  
 for (213) Unknown  
 (see item 11 on  
 Err. Summary  
 Sheet)

same error

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004

TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT  
 Output Set: N:\CRF4\07232004\H922240.raw

66 <223> OTHER INFORMATION: Xaa = Fmoc-CpSar:  
 67 9-fluorenylmethoxycarbonyl-cyclopentyl sarcosine  
**W--> 69 <221> VARIANT**  
 70 <222> LOCATION: 2  
 71 <223> OTHER INFORMATION: Xaa = MeBmt:  
 72 (4R)-N-methyl-4-butenyl-4-methyl-L-threonine  
**W--> 74 <221> VARIANT**  
 75 <222> LOCATION: 3  
 76 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid  
**W--> 78 <221> VARIANT**  
 79 <222> LOCATION: 4  
 80 <223> OTHER INFORMATION: Xaa = Sar: sarcosine  
**W--> 82 <221> VARIANT**  
 83 <222> LOCATION: 5, 7, 10, 11  
 84 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine  
**W--> 86 <221> VARIANT**  
 87 <222> LOCATION: (9)...(9)  
 88 <223> OTHER INFORMATION: Xaa = D-Ala: D-alanine  
**W--> 90 <221> VARIANT**  
 91 <222> LOCATION: (12)...(12)  
 92 <223> OTHER INFORMATION: Xaa = Valinol ester  
**W--> 94 <400> 2**  
**W--> 95 Xaa Xaa Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa Xaa**  
 96 1 5 10  
 99 <210> SEQ ID NO: 3  
 100 <211> LENGTH: 11  
 101 <212> TYPE: PRT  
 102 <213> ORGANISM: Unknown  
 104 <220> FEATURE:  
 105 <223> OTHER INFORMATION: Peptide  
**W--> 107 <221> NAME/KEY: VARIANT**  
 108 <222> LOCATION: 1  
 109 <223> OTHER INFORMATION: Xaa = Me-CpSar: methyl-cyclopentyl sarcosine  
**W--> 111 <221> VARIANT**  
 112 <222> LOCATION: 2  
 113 <223> OTHER INFORMATION: Xaa = MeBmt:  
 114 (4R)-N-methyl-4-butenyl-4-methyl-L-threonine  
**W--> 116 <221> VARIANT**  
 117 <222> LOCATION: 3  
 118 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid  
**W--> 120 <221> VARIANT**  
 121 <222> LOCATION: 4  
 122 <223> OTHER INFORMATION: Xaa = Sar: sarcosine  
**W--> 124 <221> VARIANT**  
 125 <222> LOCATION: 5, 7, 10  
 126 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine  
**W--> 128 <221> VARIANT**  
 129 <222> LOCATION: (11)...(11)  
 130 <223> OTHER INFORMATION: Xaa = MeLeu-(OH): hydroxyl-N-methylleucine

what about Xaa  
 at location 9?  
 (see p. 3)

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004  
TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT  
Output Set: N:\CRF4\07232004\H922240.raw

W--> 132 <400> 3  
W--> 133 Xaa Xaa Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa  
134 1 5 10

**RAW SEQUENCE LISTING ERROR SUMMARY** DATE: 07/23/2004  
**PATENT APPLICATION: US/08/922,240** TIME: 13:24:43

Input Set : A:\APBI-P01-007.TXT  
Output Set: N:\CRF4\07232004\H922240.raw

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1, 2, 3, 5, 7, 8, 9, 10  
Seq#:2; Xaa Pos. 1, 2, 3, 4, 5, 7, 9, 10, 11, 12  
Seq#:3; Xaa Pos. 1, 2, 3, 4, 5, 7, 9, 10, 11

VERIFICATION SUMMARY  
PATENT APPLICATION: US/08/922,240

DATE: 07/23/2004  
TIME: 13:24:43

Input Set : A:\APBI-P01-007.TXT  
Output Set: N:\CRF4\07232004\H922240.raw

L:31 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0  
L:64 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:69 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:74 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:78 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:86 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:90 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:94 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
L:107 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:111 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:120 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:124 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0